20.064

Tularemia - possible increase and new risk factors

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Purpose: Tularemia is a zoonotic disease caused by the bacterium *Francisella tularensis*. In Europe each year approximately 1200 human cases are reported. Four subspecies are currently known: *tularensis* (the most virulent form), *holarctica* (the most widespread form), *mediasiatic*, and *novicida*. In Austria *Francisella tularensis* supsp. *holarctica* is endemic in the eastern part of the country (Lower Austria and Burgenland), and is known to have a 5-year cycle. Zoonotic transmission from pet species in Europe has only been described in Norway due to a cat bite, as well as after an accidental exposure to the disease while spaying a cat. In 2014 first reports of clinically ill dogs were reported from Norway.

Methods & Materials: As hunting with dogs has a long tradition in Austria, and as there are endemic areas for the disease a first serological screening of 80 hunting dogs used in the hunt for European brown hares (*Lepus europaeus*) was conducted.

Results: Of these 80 dogs 5 tested positive for tularemia (6.25%, CI 2.1% - 14%). One positive dog had shown some clinical symptoms, however this female dog also tested positive for *Brucella canis*.

Conclusion: This result shows that dogs not only have contact to the pathogen, but also seroconvert. The occurrence of the disease is thought to increase in the next years due to our changing climate, and this year there is a new hotspot of the disease in Austria (i.e. Salzburg). These changes, as well as the result of this study highlight the need to raise the awareness level of the disease, its possible increase and new risk factors.

https://doi.org/10.1016/j.ijid.2018.11.155

20.065

Evidence of filovirus and henipavirus in bats and bat harvesters, India

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Purpose: Bats are reservoirs of several medically-important viruses. There has been little research on bat-borne viruses in India. The northeast state of Nagaland in India is a mountainous region where bushmeat is a key source of protein. Bats are hunted by several groups there and this provides an opportunity for cross-species transmission.

Methods & Materials: Our work examines sites with intense human-bat interfaces, such as traditional bat harvests in India. Here we collected 121 serum samples from three species of bats harvested from across the region and 85 human serum samples from individuals who participate in the traditional bat harvest. We also collected several tissue samples from the bats collected at the harvest. Sera were screened with a multiple serological assays for antibodies against medically henipaviruses and several members of the family filoviridae. Bat kidney, lung, and spleen tissues were pooled and tested with a pan-filovirus PCR and a pan-paramyxovirus PCR.

Results: All bat tissues were PCR-negative for filoviruses, but there were paramyxovirus positive samples. All three species of bats were seropositive for filoviruses and paramyxoviruses, while there were human sera samples that were serologically positive for filoviruses.

Conclusion: This study demonstrates that there likely has been exposure of humans to filoviruses.

https://doi.org/10.1016/j.ijid.2018.11.156

20.066

First whole genome sequence of Nipah virus from *Pteropus lylei*, Thailand

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Purpose: Nipah virus (NiV), a paramyxovirus, causes febrile encephalitis and severe respiratory disease in humans and animals. Nipah virus outbreaks have been reported from Malaysia, Bangladesh, India and Singapore. The case positive in humans have been attributed to zoonotic transmission from pigs and bats, human-to-human transmission, and eating fruits or juices contaminated with bat secretions. At present no vaccines or drugs are available for those infected with NiV. Fruit bats of family Pteropodidae have been identified as the reservoir for NiV. Whole genome Nipah virus can be help in understanding the epidemiology, evolution and origin of this virus.

Methods & Materials: The first whole genome of NiV from pooled urine of *Pteropus lylei* bat (flying fox in the Pteropodidae family) was sequenced using Next generation sequencing in Thailand. The total read of MiSeq sequencer was 19.8 Gb, where sequences of Pteropus host genome were removed, and NiV was identified using virus sequences from NCBI database.

Results: The 4,735 sequences mapped to reference generated 18,236 nucleotides, and average depth of coverage was 41.67% for NiV from Bangladesh 2004 (GenBank accession number: AY988601.1). The genome shared greater than 99% identity (18084/18236 nucleotides) with NiV isolated from a patient in Bangladesh in 2004 (AY988601.1) and 92% identity with NiV